

Amendments to the Claims:

Please **cancel** claim 44 without prejudice to or disclaimer of the underlying subject matter, **amend** claims 45-49 as shown below, and **add** new claims 92-112:

1-38. (Cancelled)

39. (Previously Presented) A DNA construct comprising a coding sequence for a *Cuphea* KAS factor A protein, and one or more coding sequences for a plant medium-chain thioesterase protein.

40. (Previously Presented) The DNA construct according to claim 39, wherein said one or more coding sequences for a plant medium-chain thioesterase protein are selected from the group consisting of *Cuphea hookeriana* FatB2, *Cuphea pulcherrima* FatB1, and *Umbellularia californica* FatB1.

41. (Previously Presented) The DNA construct according to claim 39, wherein said coding sequence for a *Cuphea* KAS factor A protein is set forth in a sequence selected from the group consisting of SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 13, and SEQ ID NO: 15.

42. (Previously Presented) The DNA construct according to claim 39, wherein said coding sequence for a *Cuphea* KAS factor A protein is set forth in SEQ ID NO: 5.

43. (Previously Presented) A DNA construct comprising a coding sequence for a *Cuphea* KAS factor A protein, and a coding sequences for *Garcinia mangostana* FatA1 thioesterase protein.

44. (Cancelled)

45. (Currently Amended) The method of Claim [[44]] 112 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein.

46. (Currently Amended) The method of Claim [[44]] 112 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea pulcherrima* FatB1 protein.

47. (Currently Amended) The method of Claim [[44]] 112 wherein said one or more plant medium-chain thioesterase proteins is an *Umbellularia californica* FatB1 protein.
48. (Currently Amended) The method of Claim [[44]] 112 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein and a *Cuphea pulcherrima* FatB1 protein.
49. (Currently Amended) The method of Claim [[44]] 112 wherein said plant synthase factor protein is a KAS factor A protein from a *Cuphea* species.
50. (Previously Presented) The method of Claim 49 wherein said *Cuphea* species is *C. hookeriana* or *C. pulcherrima*.
51. (Previously Presented) The method of Claim 50 wherein said KAS factor A protein comprises a coding sequence as set forth in SEQ ID NO:5.
52. (Previously Presented) The method of Claim 50 wherein said KAS factor A protein comprises a coding sequence encoding an amino acid sequence as set forth in SEQ ID NO:6.
53. (Previously Presented) The method of Claim 50 wherein said synthase factor A protein comprises a coding sequence encoding an amino acid sequence set forth in residues 125-466 of SEQ ID NO:6.
54. (Previously Presented) A method of altering the medium-chain fatty acid composition in plant seeds expressing one or more heterologous plant medium-chain thioesterase proteins, wherein said method comprises
- providing for expression of a plant synthase factor protein heterologous to said transgenic plant in conjunction with expression of a plant medium-chain thioesterase protein heterologous to said transgenic plant, whereby the composition of medium-chain fatty acids produced in said seeds is modified as compared to the composition of medium-chain fatty acids produced in seeds expressing said plant medium-chain thioesterase protein in the absence of expression of said plant synthase factor protein.

55. (Previously Presented) The method of Claim 54 wherein said one or more heterologous plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein.
56. (Previously Presented) The method of Claim 54 wherein said one or more heterologous plant medium-chain thioesterase proteins is a *Cuphea pulcherrima* FatB1 protein.
57. (Previously Presented) The method of Claim 54 wherein said one or more heterologous plant medium-chain thioesterase proteins is a *Umbellularia californica* FatB1 protein.
58. (Previously Presented) The method of Claim 54 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein and a *Cuphea pulcherrima* FatB1 protein.
59. (Previously Presented) The method of Claim 54 wherein said plant synthase factor protein is a KAS factor A protein from a *Cuphea* species.
60. (Previously Presented) The method of Claim 59 wherein said *Cuphea* species is *C. hookeriana* or *C. pulcherrima*.
61. (Previously Presented) The method of Claim 54 wherein said fatty acid composition is enriched for C10 fatty acids.
62. (Previously Presented) The method of Claim 54 wherein said fatty acid composition is enriched for C12 fatty acids.
63. (Previously Presented) The method of Claim 54 wherein said fatty acid composition is enriched for at least one medium chain fatty acid and at least one other medium chain fatty acid is decreased.
64. (Previously Presented) The method of Claim 63 wherein said enriched fatty acid is C12 and said decreased fatty acid is C14.

65. (Previously Presented) The method of claim 54, wherein said altered fatty acid composition comprises an increased ratio of C10 fatty acids to C8 fatty acids.
66. (Previously Presented) The method of claim 54, wherein said altered fatty acid composition comprises an increased total content of C10 fatty acids and C8 fatty acids.
67. (Previously Presented) A transformed plant comprising a coding sequence for a thioesterase protein, and a coding sequence for a KAS factor A protein, wherein said coding sequence for a KAS factor A protein is derived from a species from the genus *Cuphea*.
68. (Previously Presented) The transformed plant of claim 67, wherein said thioesterase protein is selected from the group consisting of *Cuphea hookeriana* FatB2, *Cuphea pulcherrima* FatB1, *Umbellularia californica* FatB1, and *Garcinia mangostana* FatA1.
69. (Previously Presented) The transformed plant of claim 67, wherein said thioesterase protein is *Cuphea hookeriana* FatB2.
70. (Previously Presented) The transformed plant of claim 67, wherein said thioesterase protein is *Cuphea pulcherrima* FatB1.
71. (Previously Presented) The transformed plant of claim 67, wherein said thioesterase protein is *Umbellularia californica* FatB1.
72. (Previously Presented) The transformed plant of claim 67, wherein said coding sequence for said KAS factor A protein is set forth in a sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:13 and SEQ ID NO:15.
73. (Previously Presented) The transformed plant of claim 67, wherein said coding sequence for said KAS factor A protein is set forth in SEQ ID NO:5.
74. (Previously Presented) The transformed plant of claim 67, wherein said KAS factor A protein has the amino acid sequence set forth in a sequence selected from the group consisting of SEQ ID NO:6, residues 125-466 of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:14, and residues 127-546 of SEQ ID NO:14.

75. (Previously Presented) The transformed plant of claim 67, wherein said KAS factor A protein has the amino acid sequence set forth in SEQ ID NO:6.
76. (Previously Presented) The transformed plant of claim 67, wherein said KAS factor A protein has the amino acid sequence set forth in residues 125-466 of SEQ ID NO:6.
77. (Previously Presented) The transformed plant of claim 67, wherein said transformed plant has an altered composition of medium-chain fatty acids relative to an untransformed plant.
78. (Previously Presented) The transformed plant of claim 77, wherein said fatty acid composition is enriched for C10 fatty acids.
79. (Previously Presented) The transformed plant of claim 77, wherein said fatty acid composition is enriched for C12 fatty acids.
80. (Previously Presented) The transformed plant of claim 77, wherein said fatty acid composition is enriched for at least one medium chain fatty acid and at least one other medium chain fatty acid is decreased.
81. (Previously Presented) The transformed plant of claim 77, wherein said enriched fatty acid is C12 and said decreased fatty acid is C14.
82. (Previously Presented) The transformed plant of claim 77, wherein said transformed plant has an increased ratio of C10 fatty acids to C8 fatty acids relative to an untransformed plant.
83. (Previously Presented) The transformed plant of claim 77, wherein said transformed plant has an increased total content of C10 fatty acids and C8 fatty acids relative to an untransformed plant.
84. (Previously Presented) A transformed plant comprising a coding sequence for a *Cuphea hookeriana* FatB2, a coding sequence for a *Cuphea pulcherrima* FatB1, and a coding

sequence for a KAS factor A protein, wherein said coding sequence for a KAS factor A protein is derived from a species from the genus *Cuphea*.

85. (Previously Presented) The transformed plant of claim 84, wherein said transformed plant has an altered composition of medium-chain fatty acids relative to an untransformed plant.

86. (Previously Presented) The transformed plant of claim 85, wherein said fatty acid composition is enriched for C10 fatty acids.

87. (Previously Presented) The transformed plant of claim 85, wherein said fatty acid composition is enriched for C12 fatty acids.

88. (Previously Presented) The transformed plant of claim 85, wherein said fatty acid composition is enriched for at least one medium chain fatty acid and at least one other medium chain fatty acid is decreased.

89. (Previously Presented) The transformed plant of claim 85, wherein said enriched fatty acid is C12 and said decreased fatty acid is C14.

90. (Previously Presented) The transformed plant of claim 85, wherein said transformed plant has an increased ratio of C10 fatty acids to C8 fatty acids relative to an untransformed plant.

91. (Previously Presented) The transformed plant of claim 85, wherein said transformed plant has an increased total content of C10 fatty acids and C8 fatty acids relative to an untransformed plant.

92. (New) An isolated polynucleotide comprising SEQ ID NO: 13 or complement thereof.

93. (New) The isolated polynucleotide of claim 92 consisting of SEQ ID NO:13.

94. (New) An isolated polynucleotide encoding a polypeptide sequence of SEQ ID NO: 14.

95. (New) The isolated polynucleotide of claim 94, wherein said polynucleotide comprises the sequence of SEQ ID NO: 13.
96. (New) A recombinant nucleic acid construct comprising a promoter functional in a host cell operably linked to a nucleic acid sequence of SEQ ID NO: 13.
97. (New) The recombinant nucleic acid construct according to claim 96, wherein said nucleic acid sequence is operably linked in an orientation relative to said promoter selected from the group consisting of sense and antisense.
98. (New) The recombinant nucleic acid construct according to claim 97, wherein said nucleic acid sequence is operably linked to a second recombinant nucleic acid construct having a second nucleic acid sequence encoding a desaturase enzyme.
99. (New) The recombinant nucleic acid construct according to claim 98, wherein said second nucleic acid sequence encoding a desaturase enzyme encodes a delta-9 desaturase enzyme.
100. (New) A host cell having a heterologous nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO: 13.
101. (New) The host cell of claim 100, wherein said heterologous nucleic acid molecule comprises a promoter functional in a host cell.
102. (New) The host cell of claim 100, wherein said host cell is present in a plant.
103. (New) The host cell of claim 100, wherein said host cell is present in a plant seed.
104. (New) A host cell modified by introducing a nucleic acid construct comprising a promoter functional in a host cell operably linked to the nucleic acid sequence of SEQ ID NO: 13.
105. (New) The host cell of claim 104, wherein said host cell is a plant host cell.

106. (New) A transgenic plant, or any part thereof, having a cell having a heterologous nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO: 13.

107. (New) The transgenic plant, or any part thereof of claim 106, wherein said heterologous nucleic acid molecule comprises a promoter functional in said cell.

108. (New) The transgenic plant, or any transgenic part thereof of claim 106, wherein said transgenic plant is selected from the group consisting of soybean and corn.

109. (New) A transgenic plant, or any part thereof, comprising a cell modified by introducing a nucleic acid construct comprising a promoter functional in a host cell operably linked to the nucleic acid sequence of SEQ ID NO: 13.

110. (New) The transgenic plant, or any transgenic part thereof, of claim 109, wherein said transgenic plant is selected from the group consisting of soybean and corn.

111. (New) A transgenic seed comprising a cell having a heterologous nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO: 13.

112. (New) A method for producing medium-chain fatty acids in transgenic plant seeds by expression of one or more plant medium-chain thioesterase proteins heterologous to said transgenic plant, comprising expression of a plant synthase factor protein heterologous to said transgenic plant in conjunction with expression of said one or more plant medium-chain thioesterase proteins, whereby the percentage of medium-chain fatty acids produced in seeds expressing both a plant synthase factor protein and one or more plant medium-chain thioesterase proteins is increased as compared to the percentage of medium-chain fatty acids produced in seeds expressing only said one or more plant medium-chain thioesterase proteins.